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WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID

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NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID  
NO:515 or SEQ ID NO:517, over a region of at least about 20, 30, 40, 50, 60, 75 or 100  
residues, wherein the nucleic acid encodes at least one polypeptide having a glucanase  
25 activity, and the sequence identities are determined by analysis with a sequence comparison  
algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the  
sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%,  
30 61%, 62%, 63% or 64%.

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3. The isolated or recombinant nucleic acid of claim 2, wherein the sequence identity is at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity.

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4. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

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5. The isolated or recombinant nucleic acid of claim 3, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID

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6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, 5 SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID 10 NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID 15 NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, 20 SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, 25 SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, 30 SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312,

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20 SEQ ID NO:504, SEQ ID NO:506, SEQ ID NO:508, SEQ ID NO:510, SEQ ID NO:512,  
SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518.

7. The isolated or recombinant nucleic acid of claim 1, wherein the  
sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting  
25 is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein the  
glucanase activity comprises an endoglucanase activity.

30 9. The isolated or recombinant nucleic acid of claim 1, wherein the  
glucanase activity comprises catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages or

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internal  $\beta$ -1,3-glucosidic linkages, or, hydrolyzing a glucan to produce a smaller molecular weight polysaccharide or oligomer.

10. The isolated or recombinant nucleic acid of claim 8, wherein the  
5 endoglucanase activity comprises an endo-1,4-beta-endoglucanase activity.

11. The isolated or recombinant nucleic acid of claim 10, wherein the 1,4-beta-D-glycosidic linkage activity comprises hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal.

10

12. The isolated or recombinant nucleic acid of claim 11, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

15

13. The isolated or recombinant nucleic acid of claim 11, wherein the cereal comprises a beta-D-glucan or a xyloglucan.

14. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity comprises hydrolyzing polysaccharides comprising 1,4- $\beta$ -glycoside-linked D-glucopyranoses.

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15. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity comprises hydrolyzing a cellulose, a cellulose derivative or a hemicellulose.

25

16. The isolated or recombinant nucleic acid of claim 15, wherein the glucanase activity comprises hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product.

30

17. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity comprises catalyzing hydrolysis of glucan in a feed, a food product or a beverage.

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18. The isolated or recombinant nucleic acid of claim 17, wherein the feed, food product or beverage comprises a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable.

5 19. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity comprises catalyzing hydrolysis of a glucan in a microbial cell, a fungal cell, a mammalian cell or a plant cell.

10 20. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity is thermostable.

15 21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a glucanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C.

20 22. The isolated or recombinant nucleic acid of claim 1, wherein the glucanase activity is thermotolerant.

25 23. The isolated or recombinant nucleic acid of claim 22, wherein the polypeptide retains a glucanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

30 24. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55,

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- SEQ ID NO:381, SEQ ID NO:383, SEQ ID NO:385, SEQ ID NO:387, SEQ ID NO:389,  
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SEQ ID NO:411, SEQ ID NO:413, SEQ ID NO:415, SEQ ID NO:417, SEQ ID NO:419,  
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10 SEQ ID NO:471, SEQ ID NO:473, SEQ ID NO:475, SEQ ID NO:477, SEQ ID NO:479,  
SEQ ID NO:481, SEQ ID NO:483, SEQ ID NO:485, SEQ ID NO:487, SEQ ID NO:489,  
SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID NO:497, SEQ ID NO:499,  
SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509,  
SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517, wherein the nucleic  
15 acid encodes a polypeptide having a glucanase activity.

25. The isolated or recombinant nucleic acid of claim 24, wherein the  
nucleic acid is at least about 20, 30, 40, 50, 60, 75, 100, 150, 200, 300, 400, 500, 600, 700,  
800, 900, 1000 or more residues in length or the full length of the gene or transcript.

20

26. The isolated or recombinant nucleic acid of claim 24, wherein the  
stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of  
about 65°C for about 15 minutes.

25

27. A nucleic acid probe for identifying a nucleic acid encoding a  
polypeptide with a glucanase activity, wherein the probe comprises at least 10 consecutive  
bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,  
SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID  
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30 SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID  
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NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID  
NO:517, wherein the probe identifies the nucleic acid by binding or hybridization.

15

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

20

29. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a glucanase activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19,  
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NO:487, SEQ ID NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID NO:495, SEQ ID  
NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID  
NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID  
10 NO:517, wherein the sequence identities are determined by analysis with a sequence  
comparison algorithm or by visual inspection.

30. The nucleic acid probe of claim 29, wherein the probe comprises an  
oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to  
15 80, about 60 to 100, or about 50 to 150 consecutive bases.

31. An amplification primer pair for amplifying a nucleic acid encoding a  
polypeptide having a glucanase activity, wherein the primer pair is capable of amplifying a  
nucleic acid comprising a sequence as set forth in claim 1 or claim 24, or a subsequence  
20 thereof.

32. The amplification primer pair of claim 31, wherein a member of the  
amplification primer sequence pair comprises an oligonucleotide comprising at least about 10  
to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22,  
25 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

33. An amplification primer pair, wherein the primer pair comprises a first  
member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18,  
19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of SEQ ID NO:1, SEQ ID  
30 NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ  
ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25,  
SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID

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NO:493, SEQ ID NO:495, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID  
15 NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID  
NO:513, SEQ ID NO:515 or SEQ ID NO:517, and a second member having a sequence as set  
forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,  
28, 29, 30 or more residues of the complementary strand of the first member.

20 34. A glucanase-encoding nucleic acid generated by amplification of a  
polynucleotide using an amplification primer pair as set forth in claim 33.

25 35. The glucanase-encoding nucleic acid of claim 34, wherein the  
amplification is by polymerase chain reaction (PCR).

36. The glucanase-encoding nucleic acid of claim 34, wherein the nucleic  
acid generated by amplification of a gene library.

30 37. The glucanase-encoding nucleic acid of claim 34, wherein the gene  
library is an environmental library.

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38. An isolated or recombinant glucanase encoded by a glucanase-encoding nucleic acid as set forth in claim 34.

39. A method of amplifying a nucleic acid encoding a polypeptide having  
5 a glucanase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

40. An expression cassette comprising a nucleic acid comprising a  
10 sequence as set forth in claim 1 or claim 24.

41. A vector comprising a nucleic acid comprising a sequence as set forth  
in claim 1 or claim 24.

15 42. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

20 43. The cloning vehicle of claim 42, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

25 44. The cloning vehicle of claim 42, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

45. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

30 46. A transformed cell comprising an expression cassette as set forth in claim 40.

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47. The transformed cell of claim 40, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

48. A transgenic non-human animal comprising a sequence as set forth in  
5 claim 1 or claim 24.

49. The transgenic non-human animal of claim 48, wherein the animal is a mouse.

10 50. A transgenic plant comprising a sequence as set forth in claim 1 or  
claim 24.

15 51. The transgenic plant of claim 50, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

52. A transgenic seed comprising a sequence as set forth in claim 1 or  
claim 24.

20 53. The transgenic seed of claim 52, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

25 54. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

30 55. The antisense oligonucleotide of claim 49, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

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56. A method of inhibiting the translation of a glucanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24.

5

57. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 24.

10 58. The double-stranded inhibitory RNA (RNAi) molecule of claim 52, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

15 59. A method of inhibiting the expression of a glucanase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 24.

20 60. An isolated or recombinant polypeptide (i) having at least 50% sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148,

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- 5 SEQ ID NO:510, SEQ ID NO:512, SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518, over a region of at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 75 or 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50% sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID  
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NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID  
NO:517, over a region of at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 75 or 100 residues,  
and the sequence identities are determined by analysis with a sequence comparison algorithm  
30 or by a visual inspection, or encoded by a nucleic acid capable of hybridizing under stringent  
conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID  
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NO:517.

20 61. The isolated or recombinant polypeptide of claim 60, wherein the  
sequence identity is over a region of at least about at least about 51%, 52%, 53%, 54%, 55%,  
56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%,  
72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,  
88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100%  
25 sequence identity.

62. The isolated or recombinant polypeptide of claim 60, wherein the  
sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100,  
150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000,  
30 1050 or more residues, or the full length of an enzyme.

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63. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316,

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SEQ ID NO:428, SEQ ID NO:430, SEQ ID NO:432, SEQ ID NO:434, SEQ ID NO:436,  
SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:442, SEQ ID NO:444, SEQ ID NO:446,  
SEQ ID NO:448, SEQ ID NO:450, SEQ ID NO:452, SEQ ID NO:454, SEQ ID NO:456,  
15 SEQ ID NO:458, SEQ ID NO:460, SEQ ID NO:462, SEQ ID NO:464, SEQ ID NO:466,  
SEQ ID NO:468, SEQ ID NO:470, SEQ ID NO:472, SEQ ID NO:474, SEQ ID NO:476,  
SEQ ID NO:478, SEQ ID NO:480, SEQ ID NO:482, SEQ ID NO:484, SEQ ID NO:486,  
SEQ ID NO:488, SEQ ID NO:490, SEQ ID NO:492, SEQ ID NO:494, SEQ ID NO:496,  
SEQ ID NO:498, SEQ ID NO:500, SEQ ID NO:502, SEQ ID NO:504, SEQ ID NO:506,  
20 SEQ ID NO:508, SEQ ID NO:510, SEQ ID NO:512, SEQ ID NO:514, SEQ ID NO:516 or  
SEQ ID NO:518.

64. The isolated or recombinant polypeptide of claim 60, wherein the  
polypeptide has a glucanase activity.

25

65. The isolated or recombinant polypeptide of claim 64, wherein the  
glucanase activity comprises an endoglucanase activity.

30

66. The isolated or recombinant polypeptide of claim 65, wherein the  
endoglucanase activity comprises an endo-1,4-beta-endoglucanase activity, or, comprises  
catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages or internal  $\beta$ -1,3-glucosidic linkages.

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67. The isolated or recombinant polypeptide of claim 66, wherein the 1,4-beta-D-glycosidic linkage activity comprises hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal.

5

68. The isolated or recombinant polypeptide of claim 67, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

69. The isolated or recombinant polypeptide of claim 67, wherein the cereal comprises a beta-D-glucan or a xyloglucan.

10

70. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises hydrolyzing polysaccharides comprising 1,4- $\beta$ -glycoside-linked D-glucopyranoses.

15

71. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises hydrolyzing a cellulose, a cellulose derivative or a hemicellulose.

20

72. The isolated or recombinant polypeptide of claim 71, wherein the glucanase activity comprises hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a paper product.

25

73. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises catalyzing hydrolysis of glucan in a feed, a food product or a beverage.

74. The isolated or recombinant polypeptide of claim 73, wherein the feed, food product or beverage comprises a cereal-based animal feed, a dough, a wort or a beer, a fruit or a vegetable.

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75. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.

5

76. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises catalyzing hydrolysis of a fermentable sugar to make a fuel product.

10

77. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity is thermostable.

15

78. The isolated or recombinant polypeptide of claim 77, wherein the polypeptide retains a glucanase activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C.

20

79. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity is thermotolerant.

25

80. The isolated or recombinant polypeptide of claim 79, wherein the polypeptide retains a glucanase activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

30

81. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and lacking a signal sequence or a prepro sequence.

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82. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and having a heterologous signal sequence or a heterologous prepro sequence.

5 83. The isolated or recombinant polypeptide of claim 64, wherein the glucanase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

10

84. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of at least half of the specific activity of the glucanase at 37°C after being heated to an elevated temperature.

15 85. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

20 86. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises at least one glycosylation site.

87. The isolated or recombinant polypeptide of claim 86, wherein the glycosylation is an N-linked glycosylation.

25 88. The isolated or recombinant polypeptide of claim 87, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

30 89. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a glucanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

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90. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a glucanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

5 91. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

92. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

10 93. The heterodimer of claim 92, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

15 94. The heterodimer of claim 92, wherein the second domain is an epitope or a tag.

95. A homodimer comprising a polypeptide as set forth in claim 60.

20 96. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60, or a subsequence thereof.

97. The immobilized polypeptide of claim 96, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

25 98. An array comprising an immobilized polypeptide as set forth in claim 60.

99. An array comprising an immobilized nucleic acid as set forth in claim 30 1 or claim 24.

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100. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60.

101. The isolated or recombinant antibody of claim 100, wherein the 5 antibody is a monoclonal or a polyclonal antibody.

102. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 60.

103. A method of isolating or identifying a polypeptide with a glucanase activity comprising the steps of:

- (a) providing an antibody as set forth in claim 100;
- (b) providing a sample comprising polypeptides; and
- (c) contacting the sample of step (b) with the antibody of step (a) under

15 conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a glucanase activity.

104. A method of making an anti-glucanase antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 24 or a 20 subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-glucanase antibody.

105. A method of making an anti-glucanase antibody comprising administering to a non-human animal a polypeptide as set forth in claim 60 or a subsequence 25 thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-glucanase antibody.

106. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid 30 comprises a sequence as set forth in claim 1 or claim 24; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

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107. The method of claim 106, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

5

108. A method for identifying a polypeptide having a glucanase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a glucanase substrate; and

10 (c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a glucanase activity.

15

109. A method for identifying a glucanase substrate comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

(b) providing a test substrate; and

20 (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a glucanase substrate.

110. A method of determining whether a test compound specifically binds 25 to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 24;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

30 (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

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111. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- 5 (a) providing a polypeptide as set forth in claim 60;  
(b) providing a test compound;  
(c) contacting the polypeptide with the test compound; and  
(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

10 112. A method for identifying a modulator of a glucanase activity comprising the following steps:

- 15 (a) providing a polypeptide as set forth in claim 64;  
(b) providing a test compound;  
(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the glucanase, wherein a change in the glucanase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the glucanase activity.

20 113. The method of claim 112, wherein the glucanase activity is measured by providing a glucanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

25 114. The method of claim 113, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a glucanase activity.

30 115. The method of claim 113, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as

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compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a glucanase activity.

116. A computer system comprising a processor and a data storage device  
5 wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 60, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

117. The computer system of claim 115, further comprising a sequence  
10 comparison algorithm and a data storage device having at least one reference sequence stored thereon.

118. The computer system of claim 117, wherein the sequence comparison  
algorithm comprises a computer program that indicates polymorphisms.  
15

119. The computer system of claim 117, further comprising an identifier  
that identifies one or more features in said sequence.

120. A computer readable medium having stored thereon a polypeptide  
20 sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

121. A method for identifying a feature in a sequence comprising the steps  
25 of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.  
30

122. A method for comparing a first sequence to a second sequence  
comprising the steps of: (a) reading the first sequence and the second sequence through use

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of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program.

123. The method of claim 122, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

10

124. The method of claim 123, further comprising an identifier that identifies one or more features in a sequence.

15 125. The method of claim 124, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a glucanase activity from an environmental sample comprising the steps of:  
20 (a) providing an amplification primer sequence pair as set forth in claim 31 or claim 33;  
(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,  
(c) combining the nucleic acid of step (b) with the amplification primer pair of  
25 step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucanase activity from an environmental sample.

30 127. The method of claim 126, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID

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NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27,  
SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID  
NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49,  
SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID  
5 NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71,  
SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID  
NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93,  
SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID  
NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID  
10 NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID  
NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID  
NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID  
NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID  
NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID  
15 NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID  
NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID  
NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID  
NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID  
NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID  
20 NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID  
NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID  
NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID  
NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID  
NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID  
25 NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID  
NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID  
NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID  
NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID  
NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID  
30 NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID  
NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID  
NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID

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NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID  
NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID  
NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID  
NO:375, SEQ ID NO:377, SEQ ID NO:379, SEQ ID NO:381, SEQ ID NO:383, SEQ ID  
5 NO:385, SEQ ID NO:387, SEQ ID NO:389, SEQ ID NO:391, SEQ ID NO:393, SEQ ID  
NO:395, SEQ ID NO:397, SEQ ID NO:399, SEQ ID NO:401, SEQ ID NO:403, SEQ ID  
NO:405, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:411, SEQ ID NO:413, SEQ ID  
NO:415, SEQ ID NO:417, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:423, SEQ ID  
NO:425, SEQ ID NO:427, SEQ ID NO:429, SEQ ID NO:431, SEQ ID NO:433, SEQ ID  
10 NO:435, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:441, SEQ ID NO:443, SEQ ID  
NO:445, SEQ ID NO:447, SEQ ID NO:449, SEQ ID NO:451, SEQ ID NO:453, SEQ ID  
NO:455, SEQ ID NO:457, SEQ ID NO:459, SEQ ID NO:461, SEQ ID NO:463, SEQ ID  
NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID  
NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID  
15 NO:485, SEQ ID NO:487, SEQ ID NO:489, SEQ ID NO:491, SEQ ID NO:493, SEQ ID  
NO:495, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID  
NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID  
NO:515 or SEQ ID NO:517, or a subsequence thereof.

20           128. A method for isolating or recovering a nucleic acid encoding a  
polypeptide with a glucanase activity from an environmental sample comprising the steps of:  
             (a) providing a polynucleotide probe comprising a sequence as set forth in  
claim 1 or claim 24, or a subsequence thereof;  
             (b) isolating a nucleic acid from the environmental sample or treating the  
25 environmental sample such that nucleic acid in the sample is accessible for hybridization to a  
polynucleotide probe of step (a);  
             (c) combining the isolated nucleic acid or the treated environmental sample of  
step (b) with the polynucleotide probe of step (a); and  
             (d) isolating a nucleic acid that specifically hybridizes with the polynucleotide  
30 probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a  
glucanase activity from an environmental sample.

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129. The method of claim 127 or claim 128, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

5 130. The method of claim 129, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

10 131. A method of generating a variant of a nucleic acid encoding a polypeptide with a glucanase activity comprising the steps of:

- (a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 24; and
- (b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

15 132. The method of claim 131, further comprising expressing the variant nucleic acid to generate a variant glucanase polypeptide.

20 133. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

25 134. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial

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gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

135. The method of claim 131, wherein the method is iteratively repeated  
5 until a glucanase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

136. The method of claim 135, wherein the variant glucanase polypeptide is  
thermotolerant, and retains some activity after being exposed to an elevated temperature.  
10

137. The method of claim 135, wherein the variant glucanase polypeptide has increased glycosylation as compared to the glucanase encoded by a template nucleic acid.

138. The method of claim 135, wherein the variant glucanase polypeptide  
15 has a glucanase activity under a high temperature, wherein the glucanase encoded by the template nucleic acid is not active under the high temperature.

139. The method of claim 131, wherein the method is iteratively repeated  
until a glucanase coding sequence having an altered codon usage from that of the template  
20 nucleic acid is produced.

140. The method of claim 131, wherein the method is iteratively repeated until a glucanase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.  
25

141. A method for modifying codons in a nucleic acid encoding a polypeptide with a glucanase activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a glucanase activity  
30 comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-Exemplary or a less Exemplary codon in the nucleic acid of step (a) and replacing it with a Exemplary or neutrally used codon encoding the same

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amino acid as the replaced codon, wherein a Exemplary codon is a codon over-represented in coding sequences in genes in the host cell and a non-Exemplary or less Exemplary codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

5

142. A method for modifying codons in a nucleic acid encoding a glucanase polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a glucanase activity comprising a sequence as set forth in claim 1 or claim 24; and,

10 (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a glucanase.

143. A method for modifying codons in a nucleic acid encoding a glucanase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a glucanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and,

20 (b) identifying a non-Exemplary or a less Exemplary codon in the nucleic acid of step (a) and replacing it with a Exemplary or neutrally used codon encoding the same amino acid as the replaced codon, wherein a Exemplary codon is a codon over-represented in coding sequences in genes in the host cell and a non-Exemplary or less Exemplary codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

25

144. A method for modifying a codon in a nucleic acid encoding a polypeptide having a glucanase activity to decrease its expression in a host cell, the method comprising the following steps:

30 (a) providing a nucleic acid encoding a glucanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and

(b) identifying at least one Exemplary codon in the nucleic acid of step (a) and replacing it with a non-Exemplary or less Exemplary codon encoding the same amino acid as

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the replaced codon, wherein a Exemplary codon is a codon over-represented in coding sequences in genes in a host cell and a non-Exemplary or less Exemplary codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

5

145. The method of claim 144, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

10 146. A method for producing a library of nucleic acids encoding a plurality of modified glucanase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

15 (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID

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25 NO:415, SEQ ID NO:417, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:423, SEQ ID  
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30 NO:465, SEQ ID NO:467, SEQ ID NO:469, SEQ ID NO:471, SEQ ID NO:473, SEQ ID  
NO:475, SEQ ID NO:477, SEQ ID NO:479, SEQ ID NO:481, SEQ ID NO:483, SEQ ID  
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NO:495, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:501, SEQ ID NO:503, SEQ ID NO:505, SEQ ID NO:507, SEQ ID NO:509, SEQ ID NO:511, SEQ ID NO:513, SEQ ID NO:515 or SEQ ID NO:517, or a subsequence thereof, and the nucleic acid encodes a glucanase active site or a glucanase substrate binding site;

- 5                   (b) providing a set of mutagenic oligonucleotides that encode naturally-  
occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,  
10                 (c) using the set of mutagenic oligonucleotides to generate a set of active site-  
encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino  
acid variations at each amino acid codon that was mutagenized, thereby producing a library  
15                 of nucleic acids encoding a plurality of modified glucanase active sites or substrate binding  
sites.

147. The method of claim 145, comprising mutagenizing the first nucleic  
acid of step (a) by a method comprising an optimized directed evolution system, Gene Site-  
15 Saturation Mutagenesis™ (GSSM™), or a synthetic ligation reassembly (SLR).

148. The method of claim 145, comprising mutagenizing the first nucleic  
acid of step (a) or variants by a method comprising error-prone PCR, shuffling,  
oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo  
20 mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble  
mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site-Saturation  
Mutagenesis™ (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

149. The method of claim 145, comprising mutagenizing the first nucleic  
acid of step (a) or variants by a method comprising recombination, recursive sequence  
recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template  
mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-  
deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion  
mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial  
30 gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a  
combination thereof.

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150. A method for making a small molecule comprising the following steps:

- (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a glucanase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;
- 5 (b) providing a substrate for at least one of the enzymes of step (a); and
- (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

10 151. A method for modifying a small molecule comprising the following steps:

- (a) providing a glucanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 24;
- 15 (b) providing a small molecule; and
- (c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the glucanase enzyme, thereby modifying a small molecule by a glucanase enzymatic reaction.

20 152. The method of claim 151, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the glucanase enzyme.

25 153. The method of claim 151, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

30 154. The method of claim 153, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

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155. The method of claim 154, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the  
5 particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

10 156. A method for determining a functional fragment of a glucanase enzyme comprising the steps of:

(a) providing a glucanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

15 (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a glucanase activity, thereby determining a functional fragment of a glucanase enzyme.

20 157. The method of claim 156, wherein the glucanase activity is measured by providing a glucanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

158. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

25 (a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

30 (d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions,

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thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

159. The method of claim 158, wherein the genetic composition of the cell  
5 is modified by a method comprising deletion of a sequence or modification of a sequence in  
the cell, or, knocking out the expression of a gene.

160. The method of claim 158, further comprising selecting a cell  
comprising a newly engineered phenotype.

10

161. The method of claim 160, further comprising culturing the selected  
cell, thereby generating a new cell strain comprising a newly engineered phenotype.

162. An isolated or recombinant signal sequence consisting of a sequence  
15 as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to  
22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33,  
1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of SEQ  
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SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID  
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NO:482, SEQ ID NO:484, SEQ ID NO:486, SEQ ID NO:488, SEQ ID NO:490, SEQ ID  
NO:492, SEQ ID NO:494, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:500, SEQ ID  
NO:502, SEQ ID NO:504, SEQ ID NO:506, SEQ ID NO:508, SEQ ID NO:510, SEQ ID  
NO:512, SEQ ID NO:514, SEQ ID NO:516 or SEQ ID NO:518; or, consisting of a sequence  
5 as set forth in Table 3.

163. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or  
10 peptide is not naturally associated with the signal peptide (SP).

164. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is not a glucanase or an endoglucanase.

15 165. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a glucanase or an endoglucanase catalytic domain (CD).

20 166. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

25 167. A method of increasing thermotolerance or thermostability of a glucanase polypeptide, the method comprising glycosylating a glucanase, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 60, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, thereby increasing the thermotolerance or thermostability of the glucanase.  
30

168. A method for overexpressing a recombinant glucanase in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or

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claim 24, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

169. A method of making a transgenic plant comprising the following steps:

5 (a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

10 170. The method as set forth in claim 169, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

15 171. The method as set forth in claim 169, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

172. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

20 (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

25 173. A method for hydrolyzing, breaking up or disrupting a glucan-comprising composition comprising the following steps:

(a) providing a polypeptide having a glucanase activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

30 (b) providing a composition comprising a glucan; and

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(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the glucanase hydrolyzes, breaks up or disrupts the glucan-comprising composition.

5

174. The method as set forth in claim 173, wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

10 175. A dough or a bread product comprising a polypeptide as set forth in claim 64.

176. A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide as set forth in claim 64 under conditions sufficient for conditioning the dough.

15

177. A beverage comprising a polypeptide as set forth in claim 64.

178. A method of beverage production comprising administration of at least one polypeptide as set forth in claim 64 to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage.

20

179. The method of claim 178, wherein the beverage or beverage precursor is a wort or a beer.

25

180. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 64.

181. A method for utilizing a glucanase as a nutritional supplement in an animal diet, the method comprising:

30 preparing a nutritional supplement containing a glucanase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 64; and

administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal.

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182. The method of claim 181, wherein the animal is a human.

5 183. The method of claim 181, wherein the animal is a human.

184. The method of claim 181, wherein the animal is a ruminant or a monogastric animal.

10 185. The method of claim 181, wherein the glucanase enzyme is prepared by expression of a polynucleotide encoding the glucanase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

15 186. The method of claim 185, wherein the organism is selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

20 187. An edible enzyme delivery matrix comprising a thermostable recombinant glucanase enzyme.

188. The edible enzyme delivery matrix of claim 187 comprising a polypeptide as set forth in claim 64.

25 189. A method for delivering a glucanase supplement to an animal, the method comprising:

preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant glucanase enzyme, wherein the pellets readily disperse the glucanase enzyme contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal.

30 190. The method of claim 189, wherein the recombinant glucanase enzyme comprises a polypeptide as set forth in claim 64.

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191. The method of claim 189, wherein the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

5 192. The method of claim 189, wherein the edible carrier comprises grain germ that is spent of oil.

10 193. The method of claim 189, wherein the glucanase enzyme is glycosylated to provide thermostability at pelletizing conditions.

194. The method of claim 189, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a glucanase.

15 195. The method of claim 189, wherein the pelletizing conditions include application of steam.

20 196. The method of claim 189, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

197. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a glucanase activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

25 198. The isolated or recombinant nucleic acid of claim 197, wherein the signal sequence is derived from another glucanase or a non-glucanase enzyme.

30 199. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a glucanase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

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200. A cellulose- or cellulose derivative- composition comprising a polypeptide as set forth in claim 64.

201. A wood, wood pulp or wood product comprising a polypeptide as set  
5 forth in claim 64.

202. A paper, paper pulp or paper product comprising a polypeptide as set forth in claim 64.

10 203. A method for reducing lignin in a paper, a wood or wood product comprising contacting the paper, wood or wood product with a polypeptide as set forth in claim 64.

15 204. A detergent composition comprising a polypeptide as set forth in claim  
64.

205. A pharmaceutical composition comprising a polypeptide as set forth in  
claim 64.

206. A method for eliminating or protecting animals from a microorganism comprising a glucan comprising administering a polypeptide as set forth in claim 64.

207. The method of claim 206, wherein the microorganism is a bacterium.

25 208. The method of claim 207, wherein the bacterium is a salmonellae.

209. A fuel comprising a polypeptide as set forth in claim 64.

210. A method for making a fuel comprising contacting a fermentable sugar  
30 with a polypeptide as set forth in claim 64.

211. A dairy product comprising a polypeptide as set forth in claim 64.

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212. The dairy product of claim 211 comprising a milk, an ice cream, a cheese or a yogurt.

5 213. A method for improving texture and flavor of a dairy product comprising the following steps: (a) providing a polypeptide of the invention as set forth in claim 64; (b) providing a dairy product; and (c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the glucanase can improve the texture or flavor of the dairy product.

10

214. An isolated or recombinant polypeptide having a sequence as set forth in claim 60 and comprising at least one amino acid residue conservative substitution.

15 215. The isolated or recombinant polypeptide of claim 214, wherein the conservative substitution comprises replacement of an aliphatic amino acid with another aliphatic amino acid; replacement of a Serine with a Threonine or vice versa; replacement of an acidic residue with another acidic residue; replacement of a residue bearing an amide group with another residue bearing an amide group; exchange of a basic residue with another basic residue; or, replacement of an aromatic residue with another aromatic residue, or a combination thereof.

20 216. The isolated or recombinant polypeptide of claim 215, wherein the aliphatic residue comprises Alanine, Valine, Leucine, Isoleucine or a synthetic equivalent thereof.

25

217. The isolated or recombinant polypeptide of claim 215, wherein the acidic residue comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof.

30 218. The isolated or recombinant polypeptide of claim 215, wherein the residue comprising an amide group comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof.

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219. The isolated or recombinant polypeptide or claim 215, wherein the basic residue comprises Lysine, Arginine or a synthetic equivalent thereof.

220. The isolated or recombinant polypeptide or claim 215, wherein the  
5 aromatic residue comprises Phenylalanine, Tyrosine or a synthetic equivalent thereof.